

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/719,755

DATE: 10/30/2001

TIME: 14:30:03

Input Set : A:\Cura-141.app

Output Set: N:\CRF3\10302001\I719755.raw

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3 <110> APPLICANT: Nandabalan, Krishnan
4   Yang, Meija
6 <120> TITLE OF INVENTION: p27(Kip-1)-FKBP-12 Protein Complexes
8 <130> FILE REFERENCE: Cura-14 US: p27(Kip-1)-FKBP-12 Complex
10 <140> CURRENT APPLICATION NUMBER: 09/719,755
11 <141> CURRENT FILING DATE: 2000-12-15
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/13659
14 <151> PRIOR FILING DATE: 1999-06-18
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 597
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(594)
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32   1               5               10               15
34 gac gcc agg cag gcg gag cac ccc aag ccc tcg gcc tgc agg aac ctc   96
35 Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
36   20               25               30
38 ttc ggc ccg gtg gac cac gaa gag tta acc cgg gac ttg gag aag cac   144
39 Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
40   35               40               45
42 tgc aga gac atg gaa gag gcg agc cag cgc aag tgg aat ttc gat ttt   192
43 Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
44   50               55               60
46 cag aat cac aaa ccc cta gag ggc aag tac gag tgg caa gag gtg gag   240
47 Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
48   65               70               75               80
50 aag ggc agc ttg ccc gag ttc tac tac aga ccc ccg cgg ccc ccc aaa   288
51 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
52   85               90               95
54 ggt gcc tgc aag gtg ccg gcg cag gag agc cag gat gtc agc ggg agc   336
55 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
56   100              105              110
58 cgc ccg gcg gcg cct tta att ggg gct ccg gct aac tct gag gac acg   384
59 Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
60   115              120              125
62 cat ttg gtg gac cca aag act gat ccg tcg gac agc cag acg ggg tta   432
63 His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
64   130              135              140
66 gcg gag caa tgc gca gga ata agg aag cga cct gca acc gac gat tct   480
67 Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser

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68 145          150          155          160
70 tct act caa aac aaa aga gcc aac aga aca gaa gaa aat gtt tca gac 528
71 Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
72          165          170          175
74 ggt tcc cca aat gcc ggt tct gtg gag cag acg ccc aag aag cct ggc 576
75 Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
76          180          185          190
78 ctc aga aga cgt caa acg taa 597
79 Leu Arg Arg Arg Gln Thr
80          195
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84 <211> LENGTH: 198
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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90 1          5          10          15
92 Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
93          20          25          30
95 Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
96          35          40          45
98 Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
99          50          55          60
101 Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
102 65          70          75          80
104 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
105          85          90          95
107 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
108          100          105          110
110 Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
111          115          120          125
113 His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
114          130          135          140
116 Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
117 145          150          155          160
119 Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
120          165          170          175
122 Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
123          180          185          190
125 Leu Arg Arg Arg Gln Thr
126          195
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131 <211> LENGTH: 582
132 <212> TYPE: DNA
133 <213> ORGANISM: Homo sapiens
135 <220> FEATURE:
136 <221> NAME/KEY: CDS
137 <222> LOCATION: (10)..(333)
139 <400> SEQUENCE: 3

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140 gccgccgcc atg gga gtg cag gtg gaa acc atc tcc cca gga gac ggg cgc 51
141      Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
142      1          5          10
144 acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc ggg atg 99
145 Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
146 15          20          25          30
148 ctt gaa gat gga aag aaa ttt gat tcc tcc cgg gac aga aac aag ccc 147
149 Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro
150          35          40          45
152 ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg gaa gaa 195
153 Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
154          50          55          60
156 ggg gtt gcc cag atg agt gtg ggt cag aga gcc aaa ctg act ata tct 243
157 Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
158 65          70          75
160 cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc cca cca 291
161 Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
162 80          85          90
164 cat gcc act ctc gtc ttc gat gtg gag ctt cta aaa ctg gaa 333
165 His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
166 95          100          105
168 tgacaggaat ggcctcctcc cttagctccc tgttcttgga tctgcctgga gggatctggt 393
170 gcctccagac atgtgcacat gatccatgat gagcttttcc tgatgttcca ctccactttg 453
172 tatagacatc tgccctgact gaatgtgttc tgtcactcag ctttgcctcc gacacctctg 513
174 tttcctcttc ccctttctcc tcgtatgtgt gtttacctaa actatatcgg ataaacctca 573
176 agttattca 582
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 108
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 4
185 Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
186 1          5          10          15
188 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
189 20          25          30
191 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
192 35          40          45
194 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
195 50          55          60
197 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
198 65          70          75          80
200 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
201 85          90          95
203 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
204 100          105
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 43
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence

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213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence:
215 oligonucleotide
217 <400> SEQUENCE: 5
218 ggactaggcc gaggtggcca tgggagtgcg ggtggaaacc atc 43
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 43
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence:
228 oligonucleotide
230 <400> SEQUENCE: 6
231 ggactaggcc tcctgggcct cattccagtt ttagaagctc cac 43

VERIFICATION SUMMARY

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